

Branching Transition of a Directed Polymer in Random Medium

Giovanni Sartoni^{1*} and Attilio L. Stella²

¹*Dipartimento di Fisica and Sezione INFN, Università di Bologna, I-40126 Bologna, Italy*

²*INFM-Dipartimento di Fisica and Sezione INFN, Università di Padova, I-35131 Padova, Italy*
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A directed polymer is allowed to branch, with configurations determined by global energy optimization and disorder. A finite size scaling analysis in 2D shows that, if disorder makes branching more and more favorable, a critical transition occurs from the linear scaling regime first studied by Huse and Henley [Phys. Rev. Lett. **54**, 2708 (1985)] to a fully branched, compact one. At criticality clear evidence is obtained that the polymer branches at all scales with dimension \bar{d}_c and roughness exponent ζ_c satisfying $(\bar{d}_c - 1)/\zeta_c = 0.13 \pm 0.01$, and energy fluctuation exponent $\omega_c = 0.26 \pm 0.02$, in terms of longitudinal distance.

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Linear directed polymers in random medium (DPRM) are a paradigmatic model [1,2], of central importance for fields like equilibrium interfaces in random ferromagnets [3] or fracture [4], in 2D, and flux lines of high- T_c superconductors [5], in 3D. The behavior of DPRM at large scales is generally controlled by properties at temperature $T = 0$, where the model reduces to an optimization problem [1,3]. Imagine we assign independently a random energy \mathcal{E}_b to each edge b of a square lattice. At $T = 0$, the optimal DPRM is the linear directed (no overhangs) path $\Pi(t)$, which covers a given distance t parallel to its direction, e.g. $(1, 1)$, and minimizes $E_\Pi = \sum_{b \in \Pi} \mathcal{E}_b$. Optimization determines a self-affine geometry of the optimal Π and a peculiar scaling of E_Π fluctuations, quite universal with respect to different forms of the environmental disorder [1].

So far, much activity on DPRM concentrated on a transition occurring in high enough D between a low- T regime with rugged free energy landscape, and an high- T one, with smooth phase space [6,1]. In the present Letter we discuss a novel critical transition, triggered by disorder alone, and occurring in an appropriate generalization of DPRM. We release the constraint of linearity and consider polymers which can form branches and loops. At the same time, we assume that the random energy \mathcal{E}_b can take both positive and negative values. We look for the branched directed polymer Π (BDPRM) spanning a certain longitudinal distance t and optimizing E_Π (defined as in the linear case). Even a very little percentage of negative energy bonds suffices now to induce branches and loops in the optimal Π , at least at small scales. Indeed, a single negative bond met along an optimal linear path can easily become a branch, if it lowers E_Π once included in Π . However, as long as the weight of negative energies in the \mathcal{E}_b -distribution remains low, the optimal Π is likely to remain linear at large scales. On the other hand, if this weight is very large, one expects branches and loops to develop wherever possible, leading to a sort of fully ramified, compact structure for Π .

For a specific model, we find here that such two limiting regimes hold on respective sides of a sharp threshold concentration of negative energy bonds. Right at threshold, a critical transition occurs, with Π characterized by a branching probability between 0 and 1 at all scales. This critical regime, with an infinite hierarchy of loops and dangling ends, is the first of this kind met in this field and demonstrates an unexpected richness of possible solutions of problems of global optimization with disorder. The transition has analogies with theta- or similar points in polymer physics.

A main motivation to study transitions like this comes from recent attempts to explain the puzzling universality of 2D random Potts ferromagnets [7]. To the purpose of evaluating its free energy, the interface between two phases of a q -state Potts model can be schematized as a directed path, which possibly includes bubbles of the other $q - 2$ phases [7]. At $T = 0$ these bubbles are induced by the presence of antiferromagnetic couplings, which naturally proliferate under renormalization. Such interfaces with bubbles are ramified polymers without dangling ends, and obey global optimization. In the ferromagnetic phase bubbles should not develop at large scales, while in the disordered phase they should form a compact "froth" structure. The existence and nature of peculiar, bubbling critical regimes for these polymers can be an important element to understand the above universality [7]. Another potential field of application are models of fracture in disordered materials [4].

Counting the configurations of a ramified structure, even if directed, is a problem of non-polynomial complexity. An additional difficulty hindering progress in these problems comes from the need of sampling adequately over disorder. Thus, our study here is based on a quite extensive computational effort, combined with a suitable choice of model and method of scaling analysis. We consider bond branched polymers directed at 45° with respect to the coordinate directions of a square lattice, with origin in O (Fig.1a). No branch can turn back-

wards with respect to the polymer direction. A polymer, $\Pi(t)$, extends from O up to the straight line, S_t , at distance t from O and orthogonal to the polymer direction (Fig. 1a). For bond energies we choose a distribution $P(\mathcal{E}_b) = p\delta(\mathcal{E}_b - 1) + (1 - p)\delta(\mathcal{E}_b + 1)$ with $0 \leq p \leq 1$ [8]. Upon decreasing p from 1, we expect to possibly meet a threshold as described above at some $p = p_c$.

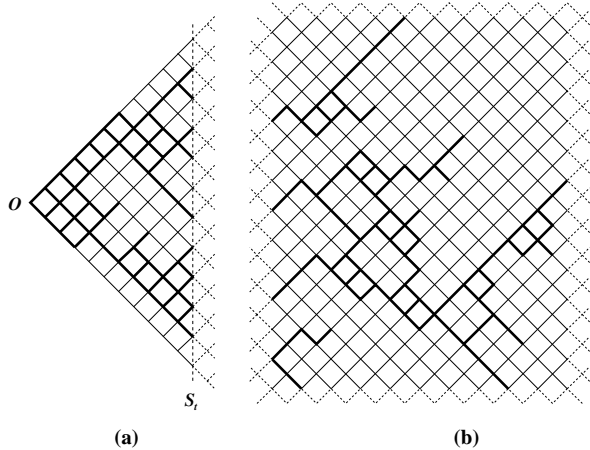


FIG. 1. (a) BDPRM configuration without strip restriction. t is the number of steps of any linear path joining O with S_t . (b) A portion ($\Delta t = 21$) of optimal BDPRM confined within a strip ($L = 13$). Disorder is generated with $p = 0.925$. Strips are periodic in the L direction.

Information on the optimal path in a given disorder configuration is transferred from t to $t + 1$ by updating the set $\{E(\tau, t)\}$ of the optimal Π energies for given t and $\tau = \Pi(t) \cap S_t$. The recursion for E reads:

$$E(\tau', t + 1) = \min_{\tau, \sigma} [E(\tau, t) + \epsilon(\sigma)] \quad (1)$$

where $\tau' = \Pi(t + 1) \cap S_{t+1}$ and $\epsilon(\sigma)$ is the energy associated to each admissible set of bonds $\sigma(\tau, \tau')$ connecting points in τ to points in τ' . There are typically several such sets for given τ and τ' . The least energy, $E_{\min}(t) = \min_{\Pi(t)} E_{\Pi(t)}$ is then calculated as $E_{\min}(t) = \min_{\tau} E(\tau, t)$. Thus, in order to identify the optimal Π , at any given t , we have to determine $E(\tau', t')$ for all $t' < t$ and $\tau' \subset S_{t'}$, consistently with eq.(1). There are $2^{t+1} - 1$ different τ intersections corresponding to all non-empty subsets of points in S_t , and altogether $2(t + 1)$ bonds connecting S_t to S_{t+1} , hence a transfer algorithm must scan $2^{2t+2} - 1$ σ -configurations to calculate the minimum in (1). This means in total $2^{3(t+1)}$ operations per t -step. Thus, as soon as t exceeds a few units, a reasonable statistics over disorder can not be collected. Clearly, one cannot simply apply the strategy of following the polymer development within the triangle in Fig.1a up to large t : a different method of scaling analysis and some restrictions on allowed configurations are in order. Thus, we confine Π within a strip of fixed width, L , and length t (Fig.1b). The t -transfer of information on optimal configurations

within such a strip has a t -independent computational cost determined by L . Our strategy is to extract information on asymptotic properties from strip calculations for relatively small L by exploiting finite size scaling [9].

Since transfer can be made much faster by restricting to only one σ the possible connections between two compatible τ and τ' in eq.(1), the following constraint is applied to determine such unique σ : BDPRM configurations are assumed to be always such to necessarily imply bond connection between neighboring sites in $\tau \subset S_t$ and in $\tau' \subset S_{t+1}$. Namely the unique σ considered in (1) is that accomplishing all possible nearest neighbor connections between the considered τ and τ' . Such restriction offers the advantage of reducing the operations necessary to determine $E(\tau', t + 1)$ in (1) by a factor 2×2^L . On the other hand, such σ represents the contribution to transfer matrix elements with the highest rate of loop and branch formation, leaving also a wide possibility of dangling ends in the structure, and thus making the model fully adequate to display the transition we are interested in. Indeed, we also performed extensive calculations for an ordered version of this restricted model at $T > 0$ to test the effects of such restriction. On strips with L up to 10, with methods similar to those in use for directed lattice animals (DA) [10], we estimated correlation length exponents $\nu_{\parallel} = 0.81 \pm 0.02$ and $\nu_{\perp} = 0.48 \pm 0.02$, to be compared with $\nu_{\parallel} = 0.818 \pm 0.001$ and $\nu_{\perp} = 1/2$ for DA [10,11]. This suggests that our model, without disorder, belongs to the same universality class as unrestricted DA.

We identify the transverse BDPRM width, at a given t , as the root mean square distance of the points in τ from the middle of the strip. Since we expect such width, averaged over random bond configurations, to grow like t^{ζ} ($0 \leq \zeta \leq 1$) on infinite lattice, crossover on our strips should be controlled by the ratio t^{ζ}/L . So, the average total number of bonds should scale with L and t as:

$$\mathcal{N}(L, t) \equiv \langle N(L, t) \rangle = t^{\bar{d}} n\left(\frac{t^{\zeta}}{L}\right) \quad (2)$$

where \bar{d} is a fractal dimension and n is a crossover function. The brackets indicate average over disorder. For $t, L \gg 1$, and $t^{\zeta} \ll L$ we should recover the behavior on unrestricted lattice. So $\lim_{x \rightarrow 0} n(x) = \text{const.} \neq 0$. On the other hand, for $t^{\zeta} \gg L$, \mathcal{N} must become proportional to t as a consequence of statistical invariance under t -translations. Thus, $n(x) \sim_{x \rightarrow \infty} x^{\frac{1-\bar{d}}{\zeta}}$. This means that $\mathcal{N}(L, t) \sim_{t \gg L} A(L)t$, with $A(L) \sim L^{(\bar{d}-1)/\zeta}$. In a similar way, for the fluctuations of optimal path energies due to lattice disorder we expect

$$\Delta \mathcal{E}(L, t) \equiv \langle (E_{\min}(t) - \langle E_{\min}(t) \rangle)^2 \rangle^{1/2} \sim t^{\omega} e\left(\frac{t^{\zeta}}{L}\right) \quad (3)$$

For $t^{\zeta} \gg L$, $\Delta \mathcal{E}$ should grow like $t^{1/2}$, as a consequence of the central limit theorem [12]. The amplitude of this

$t^{1/2}$ behavior should scale as $B(L) \sim L^{(\omega-1/2)/\zeta}$. On the other hand, for $t^\zeta \ll L$, $e \sim \text{const.}$, as ω describes $\Delta\mathcal{E}$ scaling without strip restriction. Of course, functions like n and A , and the various exponents, can depend on p .

We explored systematically the scalings in eqs.(2) and (3) for different p 's. L and t ranged up to 9 and several hundreds, respectively, and data for \mathcal{N} and $\Delta\mathcal{E}$ resulted from statistics over a minimum of 2×10^3 up to a maximum of 10^5 disorder configurations. The most convincing exponent determinations always occurred when analyzing regimes at $t^\zeta \gg L$. E.g., the amplitude $A(L, p)$ can always be estimated with good accuracy (relative error bars $< 10^{-2}$), being determined by averaging over large data sets. The trend of the effective exponents $\ln[A(L+1, p)/A(L, p)] / \ln[(L+1)/L]$ can be extrapolated rather well for all p 's (Fig.2). For $p \lesssim 0.90$ extrapolation to $(\bar{d}-1)/\zeta \simeq 1$ is always clear. This indicates a compact, fully branched regime ($\bar{d} = 2, \zeta = 1$). On the other hand, for $0.94 \lesssim p \lesssim 0.98$, we extrapolate $(\bar{d}-1)/\zeta \simeq 0$ [13]. This suggests $\bar{d} = 1$, i.e. a linear regime.

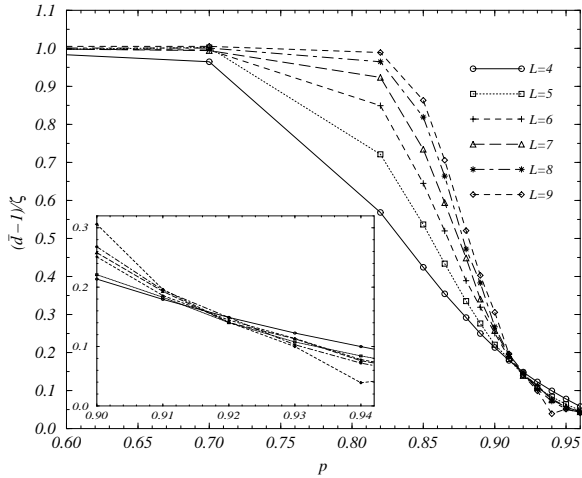


FIG. 2. Effective determinations of $(\bar{d}-1)/\zeta$ for different L and varying p . The insert shows a magnification of the transition region, where exponent curves intersect.

Most interesting, there is a narrow region ($p \sim 0.92 \div 0.93$) at which the trends of approach to the above two asymptotic values exchange each other, and intersections of effective exponent “curves” for different L concentrate and stabilize. The corresponding value $(\bar{d}_c - 1)/\zeta_c \simeq 0.12 \div 0.14$ is an obvious candidate to represent a distinct border regime right at $p = p_c \simeq 0.925$. The data in Fig.2 suggest a step at $p = p_c$ for $L \rightarrow \infty$. The scenario is further elucidated by a similar analysis of B amplitudes in eq.(3). This time we get clearly $(\omega - 1/2)/\zeta \simeq 0.50$ for $p \lesssim 0.86$ and $(\omega - 1/2)/\zeta \simeq -0.27$ for $0.94 \lesssim p \lesssim 0.98$. The value 0.50 confirms a compact, fully branched

regime, for which we expect $\zeta = 1$, and also, rather naturally, $\omega = 1$ [14]. $(\omega - 1/2)/\zeta \simeq -0.27$ in the $\bar{d} \simeq 1$ region is clear evidence of standard, linear DPRM scaling ($\omega = 1/3$, $\zeta = 2/3$ [1,3]). Thus, in this regime the presence of branchings at small scales does not change the universal behavior with respect to the strictly linear case. Unfortunately, it is more difficult to guess precisely the border-line value of $(\omega_c - 1/2)/\zeta_c$. This is probably due to the circumstance that for $p = p_c$ this combination of exponents seems to be lower than in the regimes on both sides. So, the crossover pattern can not stabilize simply and nicely as in the case of Fig.2. A direct determination of ω in the short time regime ($t \lesssim L = 9$), by fitting eq.(3) directly, gives $\omega_c = 0.26 \pm 0.02$, distinct from the DPRM $\omega = 1/3$ [15]. Assuming ζ_c equal to 1, this ω_c is consistent with our extrapolation of $(\omega_c - 1/2)/\zeta_c$ from $B(L, p_c)$ ($\omega_c = 0.27 \pm 0.02$). Further insight comes from data collapse plots testing A in the form

$$A(L, p) = L^{(\bar{d}_c - 1)/\zeta_c} a((p - p_c)L^\phi) \quad , \quad (4)$$

where ϕ is a crossover exponent (Fig.3). Eq.(4) follows from (2), once explicitated the dependence on the relevant parameter (in renormalization group (RG) sense), $p - p_c$. Over the range studied, data collapse best for $p_c = 0.927 \pm 0.005$, $(\bar{d}_c - 1)/\zeta_c = 0.13 \pm 0.01$ and $\phi = 1.00 \pm 0.02$. $a(x) = \mathcal{A}e^{-\alpha x}$ seems to be an acceptable form for the crossover function a .

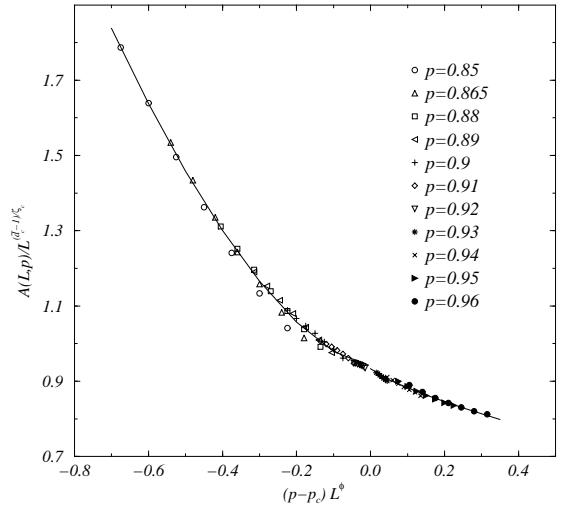


FIG. 3. Collapse plot of the rescaled mass-amplitude data.

The above analysis shows that, upon increasing the fraction of negative bond energies on the lattice, BDPRM undergo a sharp, critical transition from linear DPRM, to compact, fully branched regimes. At the transition $(\bar{d}_c - 1)/\zeta_c = 0.13 \pm 0.01$, $\omega_c = 0.26 \pm 0.02$ and $\phi = 1.00 \pm 0.02$, indicating a fractal regime, with branches on all scales, and peculiar energy fluctuations exponent. For sure \bar{d}_c , ζ_c are different from the corresponding expo-

nents of DP ($\bar{d} = 1.473 \pm 0.001$ [16], $\zeta = 0.6330 \pm 0.0008$ [17], $(\bar{d}-1)/\zeta = 0.747 \pm 0.002$), which is a reference model for a variety of phenomena, including fracture [18,19]. Our critical regime appears a peculiar result of optimization and disorder.

It is natural to ask whether the $T = 0$ behavior analyzed above should apply also at $T > 0$. A numerical investigation of $T > 0$ properties in the random case would be computationally too expensive, while higher dimensions are definitely beyond present possibilities. For $p = 1$ and $T > 0$ our model describes DA with bond fugacity $\exp(-1/T)$. Application of Harris' criterion [20] to the DA critical point ($T_c = 0.9708\dots$) suggests that disorder is relevant for our model in $2D$, because $\nu_{\parallel}[1 + (d-1)\zeta] < 2$ (see exponents quoted above). We expect a critical line joining the critical points $(1, T_c)$ and $(p_c, 0)$ on the (p, T) plane. The point $(p_c, 0)$ should be attractive from an RG point of view. Indeed, in a coarse-grained description, based on a branched path integral, for the BDPRM at $T > 0$ one would expect an elastic free energy term $-\frac{1}{T} \int \left(\frac{dx_i}{dt}\right)^2 dt$ associated with the i -th branch. This implies $dT/d\varepsilon = (1-2\bar{\zeta})T$ if t is rescaled by a factor $1 + \delta\varepsilon$ and $\bar{\zeta}$ is the roughness of a single branch. If $\bar{\zeta} > 1/2$, which is plausible in our case, irrelevance in T follows. So, the whole critical line for $p < 1$ could be controlled by the $T = 0$ fixed point tested by our scaling analysis. In higher D , while disorder should remain relevant on the basis of Harris' criterion [21], the transition of DPRM to smooth high- T free energy landscape [6] could modify the above phase diagram.

Summarizing, we gave evidence that properly chosen disorder conditions determine a branched critical regime in a generalized version of DPRM. In a previous study, a similar model without dangling ends on hierarchical lattice, displayed a strictly linear ($\bar{d}_c = 1$) $T = 0$ critical regime [7]. So, dangling ends could be essential for obtaining $\bar{d}_c > 1$ in a BDPRM model. Further clarification of this issue may be a crucial test for the scenario drawn in ref. [7], concerning the universality mechanism in random ferromagnets with several coexisting phases. However, a considerably more substantial computational effort would be required to such purpose. A comparison with DP clusters is also appropriate for our critical branched polymer. It was shown recently that the DP cluster backbone is the structure hosting and shaping (in the sense of Hurst's exponent) optimal linear paths for an extremal version of the DPRM model [22]. The branched fractal cluster identified here, is clearly different from the DP one, and originates in a complete and direct way from global optimization and disorder.

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* Present address: Instituut-Lorentz, Rijks Universiteit Leiden, 2300 RA Leiden, Nederland.

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- [14] Upon doubling its linear size, the compact structure grows into the union of 4 of the original units. Assuming weak dependence of the random energies of such units leads to $\omega = 1$.
- [15] Similar calculations for $0.94 < p < 0.97$, i.e. within the linear DPRM regime, give $\omega = 0.33 \pm 0.02$, which is consistent with the expected value. This suggests to trust our extrapolation of short t data.
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